RAW SEQUENCE LISTING

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Application Serial Number: 10/512,109
Source: PCT
Date Processed by STIC: 10/29/04

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PCT

RAW SEQUENCE LISTING   DATE: 10/29/2004
PATENT APPLICATION: US/10/512,109   TIME: 12:05:29

Input Set : **A:\38422A.txt**
Output Set: **N:\CRF4\10292004\J512109.raw**

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   5 <120> TITLE OF INVENTION: POLYPEPTIDE HAVING AN ACTIVITY TO SUPPORT PROLIFERATION OR
SURVIVAL
   6       OF HEMATOPOIETIC STEM CELL OR HEMATOPOIETIC PROGENITOR CELL, AND DNA CODING
   7       FOR THE SAME
   9 <130> FILE REFERENCE: 905WO1OP1572
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/512,109
C--> 11 <141> CURRENT FILING DATE: 2004-10-21
  11 <150> PRIOR APPLICATION NUMBER: US 60/376,001
  12 <151> PRIOR FILING DATE: 2002-04-26
  14 <160> NUMBER OF SEQ ID NOS: 49
  16 <170> SOFTWARE: PatentIn version 3.0
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  19 <211> LENGTH: 343
  20 <212> TYPE: DNA
  21 <213> ORGANISM: Mus musculus
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  28 cccggacccc cttgacccat gccctccccg gcctgtcaga acaggaggga cagaagacct   180
  30 cagctgccac ctgcccagag ccccacagct tcttcctgct cttcctcgtc accttggtcc   240
  32 ttgcggcagc caggcccagg tggcggtaac tgccccctat cccagacagt aactctgagt   300
  34 gctgcggcag ggtgcatgga ggggtccctc cctccttgag tcg                      343
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  37 <211> LENGTH: 546
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  46 gccctctcct tcctcattct tacaactgct cttggaatct gggcccagat cacacatgca   180
  48 acagagacaa aagaagtcca gagcagtctg aaggcacagc aagggcttga aattgaaatg   240
  50 tttcacatgg gctttcaaga ctcttcagat tgctgcctgt cctataactc acggattcag   300
  52 tgttcaagat ttataggtta ttttcccacc agtggtgggt gtaccaggcc gggcatcatc   360
  54 tttatcagca agaggggggtt ccaggtctgt gccaacccca gtgatcggag agttcagaga   420
  56 tgcattgaaa gattggagca aaactcacaa ccacggacct acaaacaata acatttgctt   480
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  60 ggctct                                                               546
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  64 <212> TYPE: DNA
  65 <213> ORGANISM: Mus musculus
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 86 tgaacttcat gatgacaggc tcttgggtga caattggtgc gacctttgca gccatgattg     600
 88 gagctggaat gcttgtacac tcaatatcat atgagcagag cccaggccca aagcatctgg     660
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 92 ggcctcttct cctgagagcc gcatggtaca ccgctggtat tgtgggaggc ctctctactg     780
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104 gagttgcaac tatgctagca actggaagca acagaaagaa atgaagtaac cgcttgtgat    1140
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108 cagcagaatt cccgcgcggc cgc                                            1223
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112 <212> TYPE: DNA
113 <213> ORGANISM: Mus musculus

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120 ctggcctgct ggctagttgc ccaccctgtg ggtcccgccc agagcaagga tactggagct     180
122 ttcgcctgcc tcactgagcc tgggtctcca ctccagtcat ccctccagct actttgcagc     240
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130 cagcaaagga attcctaggt ggcctgaagc gtgccaaacg acagctgtgg gaccgtacgc     480
132 ggcctgaggt acagcagtgg taccagcagt tcctctacat gggctttgat gaggctaaat     540
134 ttgaagatga tgtcaactat tggctaaaca gaaatcgaaa cggccatgac tactatggtg     600
136 actactacca gcgtcattat gatgaagatg cggccattgg tccccacagc cgggaaagct ·     660
138 tcaggcatgg agccagtgtg aactatgatg actattaagc ttcctgaggt gcccacagag     720
140 cttgtgcctg cttcagtagg ccttctctac ctataccacg tgaccatcag gctaaaggaa     780
142 agaatataag tgcttttttgc atttcatgca tgtgcttaac gatatgtctc acttaaaaa      839
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146 <211> LENGTH: 1420
147 <212> TYPE: DNA
148 <213> ORGANISM: Mus musculus

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155 ctcatggcgt tctcagcatc agtgaccttc aaacggtcct acaatgagac tgtgttctag     180
157 ctaggggtat gctgtggaaa ttcctgctac atttcatctt agtgctaaca tgtacagatt     240
159 ctgctgcgct acattcaaag ctcattactg tatatttatg ctttctctgt gtaacaagtt     300
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161 atacctgata agatgtcact ttgtttctag tgattcttaa ccatggtctg gtacatggct    360
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165 tttttggcgg gggttgggtg ggcttgattc taaccgtaag tataggataa gctagttttg    480
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169 gtcacgatac acacagagag aaagcagcat gaggcatctt gccatcagaa gccaaatttc    600
171 ttttgagtcc caaaattgat gacttatgaa atatagctga aaacaagatt tgggtgtagt    660
173 tacttgtatt tattatacaa tttccaatta catttttttt caaactcaaa ataacccatg    720
175 actttgagtg ataggtcact tggcaatgtt cttgaattac tggggagct gttgtcacta     780
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179 ctgttgaatc ggaatcaact atattagaac agaagcctga tagaagcttt ctagttaaca    900
181 cacacaaggc catggtttca aaaacatctt tgtcccctta ggtcagtttg tccttagatt    960
183 atgaattggc aggttctaat tgcattattt ccctggctga tccaggaaaa agttagaaca   1020
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187 cattggcaaa actacctctt tagcatttat gttgattcag aaacatcttg ctgatatgtg   1140
189 tagatgtttt aagcttcatt gtgaaaatat tgatgcaaga taagccatat atgaatgttg   1200
191 tattcaactt tagggcttga aattaatcct aaagtgttca cctctctcca tgtctattta   1260
193 cactctgttc ctatttacta agagggtagg ggtctcctta atatcatact tcattgttaa   1320
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197 gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa                          1420
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201 <212> TYPE: DNA
202 <213> ORGANISM: Mus musculus
204 <400> SEQUENCE: 6
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209 cgtacaatag aatccctgat ggaccgagga gccatagtga ggaacttgga aagcctgggt    180
211 gagcgtgcgc tcccctacag gatctcgagt cacagccagc agcacagccg aggagggtat    240
213 ttcctggtgg attttttatgc tccgacaagt gctgtggaga acatactgga acacttggcg    300
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219 aagaagtgag aagattcacc agattctggc cttatattta atcctaaggg cactatggt     480
221 gctgctaggt tgttgtctag gatactttag cccatgacca ttttgctgca ggaggtagaa    540
223 actgctggcc gagacctgcc ctgatgtctc tgctgagatt tcatcccact tgtgggtt      600
225 gtcgggagtg ggggtgttca cagtaccact gtagcgtttc caagagcaaa atgtttgtca    660
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232 <211> LENGTH: 1300
233 <212> TYPE: DNA
234 <213> ORGANISM: Mus musculus
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241 ggcatgggct cagcttggag gaaagtcaga ggaaattcag ataacttggt atctcttcct    180
243 gtcgttgcaa tgtttcgggg tccacttcac tatgagatac caagcagctg ccaacctcac    240
245 catactcatt tcgttacaat ttctgaggca ccgtggtgac ttgatccgac atacgaccac    300
247 gtcagttaca aaccagatct ttatggttaa cttttgaaca tttcacaaac aacattgtaa    360
249 atgtgcgatg ttatgtttta aatcagacca cagtggtccc caaatattat gtacatatga    420
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257 gttatgtagt ttcagactcc atgctgcatt ttctcttgca catgccatcc atttgcttat   660
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261 caacattacc caacaagagt gtccagtgat gaccgagtta tctcacctgc tatactttta   780
263 ctgcaataat taatgacacc tggatgagga ggcgtgcgct gacttcattg ttcacccggg   840
265 atagtgcatg agcccactga attagagctg cttctaccag caaaagtgag cagtacacat   900
267 aggtgcatgt ttgaaacatg aatcacatag agctatggag ttttgccaag tgatgtgttt   960
269 tcttttttctt ttttcttttt ttttctttttt cttcttttttt ttccttttct tcttcttctt  1020
271 ctttttttttt tttttacta tgcaaagatg ggaaatgcac aaacttccaa gacatgtctg  1080
273 aagaacttta caatacttga attttttctt taatcatccc atcacattta tggcattgat  1140
275 gcttccattg tattttttctt ttgtcccttc aacttcaatg gtttgtaatt tcaatgcaca  1200
277 acctaacttt tgtttgcagt aacttccaat cctattggct gcctggaacg gagattctgt  1260
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289 <222> LOCATION: (1)..(1671)
291 <400> SEQUENCE: 8

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293 Met Glu Leu Arg Thr Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
294 1               5                   10                  15
296 ctg gtc gtc tgc gcc cgc ggg gac ccc gcc agc aag agc cgg agc tgc    96
297 Leu Val Val Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
298             20                  25                  30
300 agc gaa gtc cgc cag atc tac ggg gct aag ggc ttt agc ctg agc gat   144
301 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
302         35                  40                  45
304 gtg ccc cag gca gag atc tcg ggt gag cac ctg cgg atc tgc ccc cag   192
305 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
306     50                  55                  60
308 ggc tac act tgc tgt acc agt gag atg gag gag aat ttg gcc aac cac   240
309 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
310 65                  70.                 75                  80
312 agc cga atg gag ctg gag agc gca ctc cat gac agc agc cgc gcc ctg   288
313 Ser Arg Met Glu Leu Glu Ser Ala Leu His Asp Ser Ser Arg Ala Leu
314                 85                  90                  95
318 cag gcc aca ctg gcc acc cag ctg cat ggc atc gat gac cac ttc cag   336
319 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
320                 100                 105                 110
322 cgc ctg ctg aat gac tcg gag cgc aca ctg cag gag gct ttc cct ggg   384
323 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Glu Ala Phe Pro Gly
324             115                 120                 125
326 gcc ttt ggg gac ctg tat acg cag aac act cgt gcc ttc cgg gac cta   432
327 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
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328     130                 135                 140
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332 145                 150                 155               160
334 gag acg ctg gcc gag ttc tgg gca cgg ctg ctg gag cgc ctc ttc aag    528
335 Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
336                 165                 170               175
338 cag ctg cac ccc cag ctg ctg cct gat gac tac ctg gac tgc ctg ggc    576
339 Gln Leu His Pro Gln Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu Gly
340                 180                 185               190
342 aag cag gcg gag gca ctg cgg ccg ttt gga gat gcc cct cga gaa ctg    624
343 Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu Leu
344         195                 200                 205
346 cgc ctg cgg gcc acc cgt gcc ttt gtg gct gca cgt tcc ttt gtg cag    672
347 Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val Gln
348         210                 215                 220
350 ggc ctg ggt gtg gcc agt gat gta gtc cgg aag gtg gcc cag gta cct    720
351 Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val Pro
352 225                 230                 235               240
354 ctg gcc cca gaa tgt tct cgg gcc atc atg aag ttg gtc tac tgt gct    768
355 Leu Ala Pro Glu Cys Ser Arg Ala Ile Met Lys Leu Val Tyr Cys Ala
356                 245                 250               255
358 cat tgc cgg gga gtc ccg ggc gcc cgg ccc tgc ccc gac tat tgc cga    816
359 His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys Arg
360                 260                 265               270
362 aat gtg ctc aaa ggc tgc ctt gcc aac cag gcc gac ctg gat gcc gag    864
363 Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala Glu
364         275                 280                 285
366 tgg agg aac ctc ctg gac tcc atg gtg ctc atc act gac aag ttc tgg    912
367 Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe Trp
368 290                 295                 300
370 ggc ccg tcg ggt gcg gag agt gtc att ggc ggt gtg cac gtg tgg ctg    960
371 Gly Pro Ser Gly Ala Glu Ser Val Ile Gly Gly Val His Val Trp Leu
372 305                 310                 315               320
374 gcg gag gcc atc aac gcc ctc cag gac aac aag gac aca ctc aca gct   1008
375 Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr Ala
376                 325                 330               335
378 aag gtc atc cag gcc tgt gga aac ccc aag gtc aat ccc cac ggc tct   1056
379 Lys Val Ile Gln Ala Cys Gly Asn Pro Lys Val Asn Pro His Gly Ser
380                 340                 345               350
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383 Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Leu Gln Glu Lys
384         355                 360                 365
386 ccc tcc aca ggt act ctg gaa aaa ctg gtc tct gag gcc aag gcc cag   1152
387 Pro Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala Gln
388         370                 375                 380
390 ctc cga gac att cag gac ttc tgg atc agc ctc cca ggg aca ctg tgc   1200
391 Leu Arg Asp Ile Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu Cys
392 385                 390                 395               400
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L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
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